

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9QYX7	PCLO_MOUSE	Mus musculus	Protein piccolo	49.148234	S518;S723;T733;S2268;S2314;T2315;T2382;T2386;T2394;T2455;S2473;S2476;T2481;S2626;S2664;T2669;T2686;T2836;T2839;S2845;S2881;T2889;T2890;T2948;S2960;S2969;T2971;T2972;T2978;S2983;S2988;S2993;S3048;T3052;T3053;S3058;T3770;T3903;S3904;S3920;T3921;S3956;S3991;S4212;S4313;S4584	S212;S844;S856;T860;T1120;S1292;S1302;S1303;S1332;S1334;S1337;S1338;S1341;S1439;S1451;S1452;S1454;S1457;S1481;S1484;S1505;S1507;T1552;S1553;S1563;S1575;S1638;T1640;S1642;S1647;S1708;S1709;T1760;S1766;S1795;S1800;S1808;S1829;S2495;T2998;S3358;S3372;T3376;T3403;S3506;S3514;S3545;S3549;S3555;S3558;S3561;S3582;S3608;S3610;S3616;S3763;S4016;S4042;S4132;S4286;S4290;S4293;S4322;S4358;S4592;S4706	34678516;22645316;19458039;16452088;22826440;33300544;22517741;26192747	MGNEASLEGEGLPEGLAAAAGGAG GSGSALHPGIPAGMEADLSQLSEEE RRQIAAVMSRAOGLPKGSVPA AAAA SPSMHRKQELDSSQAPQKQKPPDP GRPPQHGLSKSRRTDTFRSEQKLP RSPSTISLKEKSRDTFKEEYKSSMM PGFFSDVNPLSAVSSVVNKNFNPDLI SDSEAVQKQELDTTKKQKVAQKQKSE GITKPSLQOQSPKLPKQOQPGKEVIP QDIPSKSVSSQQA EKTTPQAPGTAKP SQQSPAQTPAQQA KPVAAQPGPAKA TVQQPGPAKSPAQPA GTGKSPAQPP VTAKPPAQQAGLEKTSLQQPGPKSL AQTPEGQKVPVPPGPAKSPAQQPGTAK LPAQQPGPQTAAKVPGPTKTPAQLS GPGKTPAQQPGPTKPSPPQPIPAPKQ PQQPVATKPPQPPAPAKPQPHPT PAKPQPHPTPAKPQPPQPTPAKPQ PQQTPAKPQPPQPTPAKPQPHPT PAKPQPPQPLGKPSAQQPSKISQT VTGRPLQAPPTSAQAQAPAGLSKTIC PLCNTTELLHTPEKANFNCTECQ STVCSLCGFNPNPHLTEIKEWLCN CQMQRALGGELAAIPSSPQPTPKAA SVQPATASKSPVPSQQASPKKELPSK QDSPKAPESKPPPLVKQPTLHGPTP ATAPQPPVAEALPKPAPPKPSAALP EQAKAPVADVEPKQPKTTETLTDSPS SAAATSKPAILSSVQQAQAVTTAPP LKTDSA KTSQSFPTGDTITPLDSKA MPRPASDSKIVSHPGPTSESKDPVQ KKEEPKKAQTKVTPKPDTPVVKGSP TPSGTRPTTGQATPQSQQPPKPEQS RRFSLNLGGIADAPKSQPTTPQETVT GKLFGFGASIFSQASNLISTAGQQAP HPQTGPAAPSKQAPPPSQTLLAAQGP PKSTGPHPSAPAKTTAVKKE TKGPA ENLEAKPVQAPT VVKA EKDKKPPPP KVSKPPPTPEPEKAVLAQKPKDKTKPK PACPLCRTELNVGSQDPPNFNTCTE CKNQCNCNLGCFNPTPHLTEIQEWLC LNCQTQRAISGQLGDMDKMPASS GPKASVPAPA EPPPQKTPTA AHAKG KKKETE VKAETE KQIPEKETPSIEKT PPAVATDQKLESEVTKSLVSVLPEK KPSEEEKALPADKKEKPPAAEAPPL EKKPIPDDQKLPPDAKPSASEGEEK RDLLKAHVQIPEEGPIGKVASLACEG EQQDTRPEDLPGATPQTLPKDRQK ESRDVTQPQAEGTAKEGRGEPKDR TEKEEDKSDTSSSQPKSPQGLSDT GYSSDGISGSLGEIPLIPSDEKDLLK GLKKDSFSQESSPSSPSDLAKLESTV LSILEAQASTLVGEKA EKKTPQPKVS PEQPQDQKKTQTPSETRDISISEEEI KESQEKVTSKKDSAQGFPSRKEHK ENPELVDDLSPRRASYDSVEDSSES ENSPVARRKRRTSIGSSSSEYKQED SQGSGEDED FIRKQIEMSADEDASG SEDEFIRSQLKEIGGVTESQKREET KGKGS SPAGKHRRRLTRKSSTSFDDD

AGRRHSWHDEDETFDESPELKFR
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NSTVTDKYSAESSQKKTTLYFDEEPE
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